

## Claims

1. A composition comprising at least two thermostable enzymes selected from the group consisting of endoglucanase, xylanase, phytase, protease, galactanase, mannanase, dextranase, and alpha-galactosidase, wherein each of the thermostable enzymes has a melting temperature,  $T_m$ , of at least 70°C, as determined by Differential Scanning Calorimetry (DSC) at a pH in the interval of 5.0 to 7.0.
2. The composition of claim 1, which comprises the following thermostable enzymes: (i) endoglucanase and xylanase; (ii) endoglucanase and protease; (iii) endoglucanase, xylanase and phytase; (iv) endoglucanase, xylanase and protease; (v) endoglucanase, xylanase, phytase and protease; (vi) xylanase and phytase; (vii) xylanase and protease; (viii) phytase and protease; (ix) phytase, protease and galactanase; (x) xylanase, phytase and protease; (xi) xylanase, protease and galactanase; (xii) phytase and galactanase; (xiii) galactanase and protease; (xiv) phytase, galactanase and alpha-galactosidase; (xv) phytase and alpha-galactosidase; (xvi) protease and alpha-galactosidase; (xvii) galactanase and alpha-galactosidase; (xviii) galactanase, protease and alpha-galactosidase; or (xix) at least two of endoglucanase, xylanase, phytase and galactanase.
3. The composition of any one of claims 1-3, which comprises
- (i) at least one polypeptide having xylanase activity, the polypeptide being a family 11 glycoside hydrolase; and
  - (ii) at least one polypeptide having endoglucanase activity, the polypeptide comprising
    - (a) an amino acid sequence of at least 75 % identity to amino acids 1 to 335, or 31 to 335 of SEQ ID NO:2, and/or wherein the polypeptide is
    - (b) encoded by a nucleic acid sequence which hybridizes under low stringency conditions with
      - (i) the mature endoglucanase encoding part of the plasmid contained in *Escherichia coli* DSM 14541,
      - (ii) nucleotides 1 to 1008, or 90 to 1008 of SEQ ID NO:1,
      - (iii) a subsequence of (i) or (ii) of at least 100 nucleotides, or
      - (iv) a complementary strand of (i), (ii) or (iii);
    - (c) a variant of the polypeptide having the amino acid sequence of SEQ ID NO:2 comprising a substitution, deletion, and/or insertion of one or more amino acids,
    - (d) an allelic variant of (a) or (b), or
    - (e) a fragment of (a), (b), or (d) that has endoglucanase activity.

4. The composition of claim 3, wherein
- (i) the endoglucanase and the xylanase are thermostable;
- (ii) the polypeptide having endoglucanase activity is a family 5 glycoside hydrolase;  
5 and/or
- (iii) the polypeptide having xylanase activity is derived from a strain of *Aspergillus*,  
*Bacillus*, *Humicola*, *Thermomyces*, or *Trichoderma*.
5. The composition of any one of claims 1-4, further comprising
- 10 (a) at least one fat soluble vitamin, and/or
- (b) at least one water soluble vitamin, and/or
- (c) at least one trace mineral.
6. The composition of any one of claims 1-5 which is an animal feed additive.  
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7. A method of preparing a composition of any one of claims 1-6, the method comprising the step of mixing the enzymes.
8. Use of the composition of any one of claims 1-6 in animal feed, or in the preparation  
20 of animal feed.
9. A method for improving the nutritional value of an animal feed, wherein the composition of any one of claims 1-6 is added to the feed.
- 25 10. An animal feed composition having a crude protein content of 50 to 800 g/kg and comprising the composition of any one of claims 1-6.
11. The animal feed of claim 10, which comprises at least one of soy, wheat, barley, oats  
30 or rye.
12. A method for the treatment of vegetable proteins, comprising the step of adding the composition of any one of claims 1-6 to at least one vegetable protein or protein source.
13. The method of claim 12, wherein soy, wheat, barley, oats and/or rye is included  
35 amongst the at least one vegetable protein source.